The dual role of Spn-E in supporting heterotypic ping-pong piRNA amplification in silkworms

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Running title: Spn-E facilitates heterotypic ping-pong

Abstract

The PIWI-interacting RNA (piRNA) pathway plays a crucial role in silencing transposons in the germline. piRNA-guided target cleavage by PIWI proteins triggers biogenesis of new piRNAs from the cleaved RNA fragments. This process, known as the ping-pong cycle, is mediated by the two PIWI proteins, Siwi and BmAgo3, in silkworms. However, the detailed molecular mechanism of the ping-pong cycle remains largely unclear. Here, we show that Spindle-E (Spn-E), a putative ATP-dependent RNA helicase, is essential for BmAgo3-dependent production of Siwi-bound piRNAs in the ping-pong cycle and that this function of Spn-E requires its ATPase activity. At the same time, Spn-E acts to suppress homotypic Siwi-Siwi ping-pong, but this function of Spn-E is independent of its ATPase activity. These results highlight the dual role of Spn-E in facilitating proper heterotypic ping-pong in silkworms.

Keywords: BmAgo3/ping-pong cycle/piRNA/Siwi/Spn-E

Introduction

The PIWI-interacting RNA (piRNA) pathway is a widely conserved RNA silencing mechanism against transposable elements (TEs) in the animal germline (Ozata *et al*, 2019; Wang *et al*, 2023). piRNAs are typically 24−31 nt single-stranded RNAs that guide their associated PIWI proteins to complementary target RNAs. While some PIWI proteins induce transcriptional repression in the nucleus (Aravin *et al*, 2008; Kuramochi-Miyagawa *et al*, 2008; Sienski *et al*, 2012), many PIWI proteins function as endoribonucleases and inhibit target expression by endonucleolytic cleavage in the cytoplasm (Brennecke *et al*, 2007; Gunawardane *et al*, 2007; De Fazio *et al*, 2011; Reuter *et al*, 2011).

PIWI-catalyzed target cleavage not only suppresses the target but also produces new piRNAs. In this process, known as the ping-pong cycle, the 3' fragment of PIWI-cleaved target RNA is incorporated into another PIWI as a new piRNA precursor (pre-pre-piRNA) (Ozata *et al*, 2019; Wang *et al*, 2023). The PIWI-loaded pre-pre-piRNA undergoes an additional cleavage at a downstream position by another PIWI protein or the endonuclease Zucchini (Zuc, MitoPLD in mice) to become a precursor piRNA (pre-piRNA) (Ozata *et al*, 2019; Gainetdinov *et al*, 2018; Izumi *et al*, 2020). The cleavage by Zuc not only contributes to the pre-piRNA production but also generates the 5' end of a new pre-pre-piRNA from the downstream cleavage fragment, expanding the production of phased piRNAs to the 3' direction (Mohn *et al*, 2015; Han *et al*, 2015; Ozata *et al*, 2019; Gainetdinov *et al*, 2018). In many species including silkworms, the 3' end of pre-piRNAs is further trimmed by the exonuclease Trimmer (PNLDC1 in mice) and 2'-*O*-methylated by Hen1 (HENMT1 in mice) (Nishimura *et al*, 2018; Ding *et al*, 2017;

Izumi *et al*, 2016; Zhang *et al*, 2017; Horwich *et al*, 2007; Saito *et al*, 2007; Kirino & Mourelatos, 2007). The resulting mature piRNA, in turn, guides its associated PIWI protein to cleave a complementary target RNA, thereby producing a new piRNA precursor from the opposite strand. Because PIWI proteins cleave target RNAs precisely at a position between the 10th and 11th nucleotides of the guiding piRNA, the ping-pong cycle amplifies pairs of piRNAs that have a 10-nucleotide complementary sequence at their 5' ends (Brennecke *et al*, 2007; Gunawardane *et al*, 2007; Aravin *et al*, 2008). A subset of PIWI proteins preferentially binds to piRNAs with uridine at the first nucleotide (1U) (Wang *et al*, 2023), and they produce piRNAs with an adenine bias at the 10th position (10A) by ping-pong amplification due to the nucleotide preference of the PIWI proteins in target cleavage (Wang *et al*, 2014). In silkworms, the ping-pong cycle typically occurs between the two PIWI proteins, Siwi and BmAgo3 (Kawaoka *et al*, 2009; Nishida *et al*, 2015). Siwi-bound piRNAs have a 1U and antisense bias, while BmAgo3-bound piRNAs have a 10A and sense bias (Kawaoka *et al*, 2009; Nishida *et al*, 2015).

Small RNA-guided target cleavage is a common mode of action for AGO and PIWI clades in Argonaute (Ago) family proteins (Hutvagner & Simard, 2008; Ozata *et al*, 2019). Unlike AGO proteins, however, PIWI proteins are thought to require ATP-dependent helicases for efficient release of the cleaved RNA fragments (Nishida *et al*, 2015; Murakami *et al*, 2021). So far, two ATP-dependent DEAD-box RNA helicases, Vasa and DDX43, have been proposed as the factors responsible for releasing cleavage fragments from Siwi and BmAgo3, respectively (Nishida *et al*, 2015; Murakami *et al*, 2021). Vasa-EQ, a DEAD box mutant of Vasa, lacks the ability to release ATP hydrolysis products and therefore freezes the Siwi-to-BmAgo3 ping-pong intermediate

complex (called “Amplifier”), which contains Vasa, piRNA-bound Siwi, BmAgo3, and Qin (Xiol *et al*, 2014).

piRNA pathway components often exhibit distinct patterns of cellular localization. For example, PIWI proteins and many piRNA factors (e.g., BmAgo3, Vasa) accumulate in phase-separated perinuclear granules called “nuage” (Lim & Kai, 2007; Aravin et al, 2009; Nishida et al, 2015), while other piRNA factors (e.g., Spindle-E [Spn-E], Qin) localize to another type of cytoplasmic granules known as processing bodies (P-bodies), where RNA degradation enzymes are enriched (Aravin et al, 2009; Chung et al, 2021; Standart & Weil, 2018). In addition, some piRNA processing factors (e.g. Zuc, Trimmer) are located on the mitochondrial surface through their transmembrane domains (Choi et al, 2006; Saito et al, 2010; Patil et al, 2017; Izumi et al, 2016). Their dynamic subcellular compartmentalization and coordinated actions are critical for piRNA biogenesis (Ge et al, 2019; Chung et al, 2021).

Spn-E, a DExH-box RNA helicase that also features a Tudor domain (Gillespie & Berg, 1995; Siomi *et al*, 2010), is a conserved piRNA factor essential for piRNA-mediated TE silencing (Aravin *et al*, 2001; Vagin *et al*, 2006; Shoji *et al*, 2009; Wenda *et al*, 2017; Chen *et al*, 2023). In contrast to its mouse ortholog Tdrd9, which only modestly affects the piRNA expression profile (Shoji *et al*, 2009; Wenda *et al*, 2017), Spn-E is essential for piRNA biogenesis in flies and silkworms (Vagin *et al*, 2006; Lim & Kai, 2007; Malone *et al*, 2009; Nishida *et al*, 2015). In both flies and silkworms, mutations in the ATPase domain in Spn-E fail to support the normal piRNA biogenesis and TE silencing (Ott *et al*, 2014; Nishida *et al*, 2015), indicating that ATPase activity is crucial for Spn-E function. Moreover, *spn-E* mutant flies, Aub and Ago3 are mislocalized from nuage, and the production of both sense and antisense germline

piRNAs is severely compromised (Lim & Kai, 2007; Malone *et al*, 2009), suggesting a defect in the ping-pong cycle. Silkworm Spn-E forms a complex that contains Siwi and Qin but lacks BmAgo3 and Vasa, and the depletion of Spn-E causes a reduction in Siwi- and BmAgo3-bound piRNAs (Nishida *et al*, 2015). Accordingly, a model has been proposed in which Spn-E acts in the production of Siwi-bound piRNAs independently of the ping-pong amplification (Nishida *et al*, 2015). However, the specific role of Spn-E in the piRNA biogenesis pathway remains unclear.

Here, we investigated the role of Spn-E using an ATPase-deficient mutant, Spn-E-EQ (E251Q), in BmN4 cells derived from silkworm ovaries. We observed that Spn-E-EQ forms aggregates distinct from P-bodies together with BmAgo3, and increases the precursors of Siwi-bound piRNAs. Spn-E knockdown (KD) primarily reduced Siwi-bound piRNAs generated by BmAgo3-mediated target cleavage. Wild-type Spn-E, but not the EQ mutant, could partially restore the reduction of BmAgo3-bound piRNAs, suggesting the requirement of the ATPase activity for this function of Spn-E. Unexpectedly, we also found that Spn-E KD enhances Siwi-Siwi homotypic ping-pong independently of its ATPase activity. The necessity of Spn-E for BmAgo3-dependent Siwi-bound piRNA production was further supported by artificial piRNA reporter experiments in BmN4 cells. In contrast, we found no evidence to support the requirement of DDX43 for piRNA biogenesis in cells, even though the recombinant DDX43 protein showed a robust activity to release the cleavage products of BmAgo3 in vitro. Our results suggest an essential role for Spn-E in facilitating the production of Siwi-bound piRNAs in the canonical heterotypic ping-pong cycle.

Results and Discussion

Siwi knockdown accumulates Spn-E in BmAgo3 complexes

In the ping-pong cycle of silkworms, the 3' cleavage fragments produced by BmAgo3 are loaded into Siwi as a pre-pre-piRNA and vice versa (Kawaoka *et al*, 2009; Nishida *et al*, 2015). When we analyzed immunopurified BmAgo3 complex from the lysate of Siwi KD BmN4 cells, we observed remarkable accumulation of two proteins, p160 and p40 (Fig 1A). LC-MS/MS analysis identified p160 as Spn-E, one of the conserved piRNA factors (p40 will be described elsewhere [Izumi *et al.* manuscript in preparation]). In line with the increased physical interaction, Siwi KD caused an accumulation of Spn-E in BmAgo3-containing nuage in BmN4 cells (Fig 1B). In theory, the depletion of Siwi should lead to an accumulation of BmAgo3, which remains bound to its cleavage fragments that cannot be handed over to Siwi (Nishida *et al*, 2020). Accordingly, we speculated that Spn-E functions during the handover process from BmAgo3 to Siwi in the ping-pong cycle and that Siwi KD causes Spn-E to stall at an intermediate step in this process.

ATPase-deficient Spn-E-EQ exhibits increased association with BmAgo3

Spn-E encodes a putative ATP-dependent RNA helicase belonging to the DExH-box family (Gillespie & Berg, 1995), and its ATPase activity is essential for the production of Siwi-bound piRNAs in silkworms (Nishida *et al*, 2015). To determine the process that requires the ATPase activity of Spn-E, we examined the behavior of an ATPase-deficient mutant Spn-E-EQ (E251Q). We previously reported that Spn-E localizes primarily to P-bodies (Chung *et al*, 2021), while a fraction of Spn-E partially localizes

to BmAgo3-containing nuage (Fig 1B). To minimize the effect of endogenous Spn-E, we depleted it using RNAi with double-stranded RNAs (dsRNAs) targeting the *Spn-E* 3' UTR, and complemented the cells with either wild-type Spn-E or the EQ mutant. Wild-type Spn-E exhibited a dotted distribution throughout the cytoplasm, with partial colocalization with BmAgo3-containing nuage at the perinuclear region (Fig 1C). In contrast, Spn-E-EQ formed aberrant aggregates with BmAgo3 (Fig 1C), which is reminiscent of the aggregates formed by Vasa-EQ with BmAgo3 as previously reported (Xiol *et al,* 2014). We immunoprecipitated Spn-E-EQ and confirmed that the EQ mutation of Spn-E enhances its association with BmAgo3 (Fig 1D). Because Spn-E also localizes to P-bodies (Chung *et al,* 2021), we investigated the localization of DDX6, a marker protein for P-bodies, in cells expressing Spn-E-EQ using an anti-DDX6 antibody (Fig EV1A). Although DDX6 was occasionally found near the aggregates of Spn-E-EQ and BmAgo3, it did not overlap with them (Fig EV1B). Thus, the Spn-E-EQ-BmAgo3 aggregates are probably not P-bodies themselves, but a fraction of them may fuse with P-bodies as these aggregates grow. We also examined the localization of Siwi in Spn-E-EQ expression. We found that a fraction of Siwi colocalized with the Spn-E-EQ-BmAgo3 aggregates, but to a lesser extent compared to BmAgo3 (Fig EV1C). In addition, we observed some Siwi aggregates without Spn-E and BmAgo3 (Fig EV 1C). These results suggest that the ATPase-deficient Spn-E-EQ forms an aberrant complex that is stuck with BmAgo3 and possibly with Siwi as well.

Spn-E-EQ reduces mature Siwi-bound piRNAs while accumulating their pre-piRNAs

To examine whether both Siwi and BmAgo3 are contained within the same Spn-E-EQ

complex, we performed a tandem IP experiment. We first immunoprecipitated FLAG-tagged Spn-E-EQ, and then the purified Spn-E-EQ complex was subjected to the second immunoprecipitation with anti-BmAgo3 antibody to detect the co-precipitated Siwi in the presence or absence of RNase treatment. Siwi was co-purified with BmAgo3 in the second IP and the level was largely unaffected by the RNase treatment (Fig EV1D). These results suggest that Spn-E-EQ, BmAgo3, and Siwi form an aberrantly stable complex. Given that both Siwi and BmAgo3 are co-immunoprecipitated with wild-type Spn-E albeit less strongly than Spn-E-EQ (Fig 1D), we speculate that this tertiary complex is formed at least transiently even in the normal condition.

If Spn-E uses its ATPase activity to facilitate the handover process from BmAgo3 to Siwi, the expression of Spn-E-EQ should in theory cause an accumulation of RNA fragments cleaved by BmAgo3, which would become pre-pre-piRNAs for Siwi. To explore this possibility, we attempted to detect piR1712 and piR2986, two representative Siwi-bound piRNAs generated by BmAgo3-mediated cleavage, and their precursors in BmN4 cells expressing Spn-E-EQ by northern blotting. Compared to wild-type Spn-E, Spn-E-EQ caused a reduction of mature piR1712 and piR2986 and a concomitant accumulation of longer RNA signals that correspond to the lengths of their pre-piRNAs (Fig 1E). We also observed a slight accumulation of pre-piR484, the precursor of a BmAgo3-bound piRNA, by expressing Spn-E-EQ, but the level of mature piR484 was much less affected than Siwi-bound piR1712 and piR2986 (Fig 1E). In general, pre-pre-piRNAs are cleaved at a downstream position either by Zuc or another piRNA-guided PIWI protein to become pre-piRNAs (Izumi *et al*, 2020). Unlike Zuc-mediated cleavage, the downstream cleavage by PIWI proteins can occur before pre-pre-piRNAs are loaded into new PIWI proteins. After PIWI loading, pre-piRNAs

are rapidly trimmed to the mature length, making them undetectable (Izumi *et al,* 2020). Therefore, the pre-piRNAs detected here are likely the cleavage products of downstream PIWI proteins, prior to being loaded into new PIWI proteins. Taken together, we concluded that Spn-E-EQ inhibits the handover of BmAgo3-cleaved fragments to Siwi.

Spn-E does not have an activity to release Ago3-mediated cleavage fragments

As Spn-E encodes an RNA helicase, it is conceivable that Spn-E has a function to dissociate the cleavage products from BmAgo3 to facilitate their handover to Siwi. However, DDX43, another DEAD-box RNA helicase, has been reported as the factor responsible for releasing the cleavage fragments of BmAgo3 (Murakami *et al,* 2021). To determine if Spn-E exhibits an activity similar to DDX43, we repeated the previously reported in vitro assay to examine the release of the cleavage fragments from BmAgo3. To distinguish the 5' and 3' cleavage fragments, we prepared a target RNA radiolabeled with ^{32}P at different positions and performed the in vitro target cleavage reaction using immunoprecipitated BmAgo3. After that, we added recombinant Spn-E protein (rSpn-E) or DDX43 protein (rDDX43) to the reaction and monitored the release of the cleavage fragments in the supernatant (Fig EV1E and F). Consistent with the previous report (Murakami *et al,* 2021), rDDX43 released both the 5' and 3' cleavage fragments into the supernatant (Fig EV1F). However, no such activity was detected with rSpn-E (Fig EV1F). Thus, unlike DDX43, Spn-E does not have the releasing activity for BmAgo3-cleaved RNA fragments in vitro.

To compare the effect of DDX43 dysfunction with Spn-E dysfunction on the cellular status of BmAgo3, we expressed the previously reported ATPase-deficient

mutant of DDX43, DDX43-D399A (DA), which retains the binding capacity to BmAgo3 (Murakami *et al,* 2021), in BmN4 cells and examined the localization of BmAgo3. In agreement with the previous report (Murakami *et al,* 2021), DDX43 showed dispersed expression patterns in the cytoplasm, with only occasional and partial overlapping with BmAgo3-containing nuage (Figs 1B and EV1G). This pattern was also observed with DDX43-DA (Fig EV1G). Unlike Spn-E-EQ, DDX43-DA neither formed aggregates with BmAgo3 nor affected the subcellular distribution of BmAgo3 (Fig EV1G). In addition, the expression pattern of DDX43 remained unaffected by either KD of Siwi or expression of Spn-E-EQ (Figs 1B and EV1H). Overall, DDX43 has much less impact on BmAgo3 in BmN4 cells compared to Spn-E.

Depletion of Spn-E decreases BmAgo3-dependent production of Siwi-bound piRNAs and increases the Siwi-Siwi homotypic ping-pong

We next knocked down Spn-E or DDX43 using two different dsRNAs, respectively (Fig EV2A and B) and examined the impact of KD on the piRNA expression. We first analyzed the change in the expression of piRNAs derived from TEs. While most TEs showed decreased piRNA production in Spn-E KD, a subset of TEs unexpectedly exhibited increased piRNA production (Fig EV2C, top and middle, red dots). In contrast, DDX43 KD caused little or no change in the production of TE-derived piRNAs (Fig EV2C, bottom), as previously reported (Murakami *et al,* 2021). To determine the identity of the increased piRNAs in Spn-E KD, we classified TE-mapped piRNAs into three groups according to their changes in expression, and examined their nucleotide bias for 1U and 10A, a hallmark of Siwi and BmAgo3-bound piRNAs, respectively (Figs 2A and B, and EV2D−F). We found that over half of the decreased

piRNAs in Spn-E KD are “1U but not 10A” piRNAs (Figs 2B [RNAi targeting 3' UTR] and EV2F [RNAi targeting CDS]). Moreover, our re-analysis of previously reported Siwi-IP and BmAgo3-IP piRNA libraries revealed that, as expected, these “1U but not 10A” piRNA species are predominantly bound to Siwi and that their putative partner piRNAs in the ping-pong cycle (i.e., complementary piRNAs bearing a 5' 10-nt overlapping) are predominantly bound to BmAgo3 in normal BmN4 cells (Fig EV2G, top). Therefore, Spn-E is required for the production of Siwi-bound piRNAs via BmAgo3-mediated target cleavage. On the other hand, most of the increased piRNAs in Spn-E KD have the “1U and 10A” bias (Figs 2B and EV2F). Importantly, the “1U and 10A” piRNAs and their partner piRNAs with 5' 10-nt complementarity were both concentrated in Siwi-IP (Fig EV2G, bottom), indicating that they are largely produced through a homotypic ping-pong between Siwi-Siwi.

Based on the above observation, we again categorized TE-mapped piRNAs into three different types: A→S, S→A, and S→S piRNAs (Fig 2C), where “S” and “A” represent Siwi and BmAgo3, respectively, and the arrow indicates the flow of RNA fragments during the ping-pong. For example, A→S piRNAs are predominantly bound to Siwi and have partner piRNAs with 5' 10-nt complementarity that are predominantly bound to BmAgo3 (i.e., they are Siwi-bound piRNAs produced via BmAgo3-mediated target cleavage). On the other hand, S→S piRNAs are predominantly bound to Siwi and mainly generated through the Siwi-Siwi homotypic ping-pong. We analyzed the change in the relative abundance of each piRNA type in Spn-E KD or DDX43 KD. In agreement with the analysis based on the 1U and 10A biases (Figs 2B and EV2F), A→S piRNAs were decreased and S→S piRNAs were conversely increased by Spn-E KD (Fig 2D). In contrast, DDX43 KD showed no noticeable effect on the relative

abundance for any of the groups (Fig EV2H). Thus, Spn-E, but not DDX43, is required for the BmAgo3-dependent production of Siwi-bound piRNAs and for the suppression of Siwi-Siwi homotypic ping-pong.

We next examined the requirement of the ATPase activity of Spn-E for the production of A→S piRNAs and suppression of S→S piRNAs. We constructed small RNA libraries from BmN4 cells, where endogenous Spn-E was knocked down, and either wild-type Spn-E or the ATPase-deficient mutant Spn-E-EQ was expressed. Wild-type Spn-E but not the EQ mutant partially recovered the decreased A→S piRNAs (Fig 2E), suggesting that the ATPase activity of Spn-E is required for A→S piRNA production (Fig 2F). On the other hand, the enhanced production of S→S piRNAs was rescued by the expression of both wild-type Spn-E and the EQ mutant (Fig 2E), indicating that the presence of Spn-E itself, rather than its ATPase activity, is important to repress the Siwi-Siwi homotypic ping-pong (Fig 2F).

Spn-E but not DDX43 is required for artificial A→S piRNA production

To confirm the requirement of Spn-E for *de novo* A→S piRNA production, we developed a reporter system that generates an artificial Siwi-bound piRNA, piR484-A (Figs 3A and EV3A). This reporter RNA has a target site of an abundantly expressed endogenous BmAgo3-bound piRNA and the cleavage product is expected to be loaded into Siwi via the ping-pong cycle. It also contains another downstream target site for an endogenous Siwi-bound piRNA to define the formation of the 3' end of the pre-piRNA; following the cleavage at this downstream position by Siwi, 3' end maturation by Trimmer and Hen1 is expected to occur. We co-transfected this reporter plasmid and dsRNAs targeting *Spn-E* or *DDX43* into BmN4 cells, and detected Siwi-bound piR484-

A by northern blotting. As expected, the production of piR484-A was reduced by Spn-E KD (Fig 3B). In contrast, DDX43 KD did not affect the production of piR484-A (Fig 3B), even though DDX43 mRNA was markedly decreased by KD (Fig EV3B).

We also tested another reporter that has a target site for a *piggyBac* transposon-derived piRNA, which is essentially the same as the artificial Siwi-bound piRNA reporter used in the previous study (Murakami *et al*, 2021), except that it lacks the upstream EGFP sequence (Fig 3C). Unlike the piR484-A reporter, it lacks any specific downstream piRNA target site that can define the 3' end of the pre-piRNA. To ensure that the reporter piRNA is generated even without 3' end processing, we used not only the circular plasmid but also a linearized plasmid that produces a run-off transcript with a defined 3' end. In theory, the reporter RNA transcribed from the circular plasmid is expected to have a > 60 nt sequence and the poly(A) tail downstream of the cleavage site, so the exact mechanism for the 3' end processing after Siwi-loading is unclear (Fig 3C, left). On the other hand, the BmAgo3-cleavage product of the reporter RNA transcribed from the linearized plasmid should yield a 30-nt fragment, which is expected to be loaded into Siwi as an artificial piRNA without requiring additional 3' end processing (Fig 3C, right). Similar to the result from the piR484-A system, the production of the artificial Siwi-bound piRNA was reduced by Spn-E KD, but not by DDX43 KD, for both circular and linearized plasmids (Figs 3D and EV3B). These results strongly support the requirement of Spn-E for A→S piRNA production.

To confirm the necessity of Spn-E ATPase activity for artificial Siwi-bound piRNA production, we performed a KD-rescue experiment. We co-transfected the *piggyBac* piRNA reporter plasmid and either the wild-type Spn-E or the EQ mutant-expressing plasmid, with the endogenous Spn-E knocked down. Consistent with the

analysis of endogenous piRNA expression profiles (Fig 2E), wild-type Spn-E but not the EQ mutant rescued the decrease in the artificial Siwi-bound piRNA caused by Spn-E KD (Fig 3E). Similar results were obtained with the piR484-A reporter (Fig EV3C). Taken together, we concluded that the ATPase activity of Spn-E is required for BmAgo3-dependent production of Siwi-bound piRNAs during the ping-pong cycle.

Although Spn-E has long been studied as a conserved piRNA factor, its role in piRNA biogenesis remained unclear. In this study, we showed that Spn-E is required for the BmAgo3-mediated production of Siwi-bound piRNAs in silkworms. The notable reduction of A→S piRNAs in Spn-E KD (Fig 2D) and the phenotype observed with the EQ mutant (Fig 1) strongly suggest the role for Spn-E in the ping-pong cycle. Since the expression of Spn-E-EQ increases A→S pre-piRNAs (Fig 1E), Spn-E is expected to act as an ATPase after target cleavage by BmAgo3 before the handover of the cleaved fragment to Siwi. However, as the purified Spn-E did not exhibit an activity to release the BmAgo3-mediated cleavage fragments in vitro (Fig EV1F), Spn-E is unlikely to directly dissociate the cleaved fragments from BmAgo3. Considering that Spn-E-EQ forms large aggregates with BmAgo3 (Fig 1C), we speculate that Spn-E uses its ATPase activity to dynamically regulate the dissociation of protein(s) and/or remodeling of the BmAgo3 complex on target RNAs, thereby allowing the handover of BmAgo3-cleaved fragments to Siwi. This action of Spn-E mirrors the previously discussed role of Vasa in the Siwi-to-BmAgo3 handover (Xiol *et al*, 2014). In flies, Spn-E has been implicated in the ping-pong cycle based on its germline-restricted expression and its requirement for germline piRNA production (Vagin *et al*, 2006; Lim & Kai, 2007; Malone *et al*, 2009), but its exact site of action has not been determined. Since Siwi and BmAgo3 are

orthologs of Aub and Ago3, respectively, fly Spn-E could also function in the heterotypic ping-pong from Ago3 to Aub. In our current study, we knocked down Spn-E only transiently, but a continued reduction of A→S piRNAs should inevitably lead to S→A piRNA reduction in the ping-pong cycle, ultimately causing a collapse of the entire piRNA pathway. This could explain the sterile phenotype of *spn-E* mutants in flies and silkworms (Gillespie & Berg, 1995; Stapleton *et al*, 2001; Chen *et al*, 2023).

Another ATP-dependent helicase, DDX43 was previously reported as the responsible helicase to release the cleavage fragments from BmAgo3 (Murakami *et al*, 2021). Indeed, we were able to confirm the reported activity of recombinant DDX43 protein in vitro (Fig EV1F). However, we found no evidence to support the requirement of DDX43 in A→S piRNA production in cells (Figs 3B and D, and EV2H). Further investigation is needed to clarify the biological role of DDX43.

Unexpectedly, we found that Spn-E KD hyperactivates Siwi-Siwi homotypic ping-pong and that ATPase-deficient Spn-E-EQ can rescue this phenotype (Fig 2D and E). Thus, the presence of Spn-E itself suppresses the homotypic ping-pong of Siwi independent of its ATPase activity. A similar increase of the Aub-Aub homotypic ping-pong has been reported in *qin* mutant flies (Zhang *et al*, 2011). Considering that Spn-E forms a complex with Qin and Mael and binds to unloaded Siwi (Nishida *et al*, 2015; Namba *et al*, 2022), their binding to empty Siwi may repress Siwi-Siwi homotypic ping-pong. Alternatively, but not mutually exclusively, the observed increase in S→S piRNAs by Spn-E KD may be due to an excess amount of Siwi proteins that cannot participate in heterotypic ping-pong. In either case, the dual role of Spn-E is critical to support the heterotypic ping-pong amplification of piRNAs. Of note, our analysis also revealed that the homotypic Siwi-Siwi ping-pong occurs to some extent at the basal

level in naive BmN4 cells (Fig EV2G), suggesting that it may have a biological role. Further research is required to understand the mechanistic and functional differences between the heterotypic Siwi-BmAgo3 ping-pong and homotypic Siwi-Siwi ping-pong.

Materials and Methods

Cell culture, plasmid transfection, and dsRNA transfection in BmN4 cells

BmN4 cells were cultured in IPL-41 medium (AppliChem and Hyclone) supplemented with 10% fetal bovine serum at 27 °C. Sf9 cells were cultured in Sf-900™ II SFM (Thermo Fisher Scientific/Gibco) at 28 °C on an orbital shaker platform set at 135 rpm. For immunoprecipitation experiments, a total of 4.5–6 μg of plasmid and dsRNA were transfected into BmN4 cells (~2×10^6 cells per 10 cm dish) with X-tremeGENE HP DNA Transfection Reagent (Merck Millipore/Roche). The second transfection was performed 3 days after the first transfection and the cells were harvested after an additional 5 days. For immunofluorescence experiments, a total of 0.4–0.5 μg of plasmid and dsRNAs were transfected into BmN4 cells (4–6 $\times 10^4$ cells per glass bottom 35 mm dish) with X-tremeGENE HP DNA Transfection Reagent (Merck Millipore/Roche) and cells were fixed 5–6 days later. For artificial piRNA reporter experiments, a total of 3–5 μg of plasmid and dsRNA were transfected into BmN4 cells (~2×10^6 cells per 10 cm dish) with X-tremeGENE HP DNA Transfection Reagent (Merck Millipore/Roche). Transfection was repeated 2 days and 5 days after the first transfection and the cells were harvested after an additional 4 days. For library preparation, a total of 5 μg of plasmid and dsRNA were transfected into BmN4 cells (8 $\times 10^5$ cells per 10 cm dish) with X-tremeGENE HP DNA Transfection Reagent (Merck Millipore/Roche) every 3 days four times. dsRNA preparation was described previously (Izumi *et al*, 2020). Template DNAs were prepared by PCR using primers containing T7 promoter listed in Table EV1.

Plasmid construction

pIExZ-FLAG-Spn-E was described previously (Chung *et al*, 2021). pIExZ-FLAG-Spn-E-E251Q was generated by site-directed mutagenesis.

pIEx-FLAG-DDX43, pIExZ-HA-DDX43

FLAG-tagged or HA-tagged cDNA fragment of DDX43 was amplified by RT-PCR from total RNA of silkworm ovaries and cloned into pIEx-1 vector (Merck Millipore/Novagen) or pIExZ vector by In-fusion cloning kit (Takara).

pCold-DDX43, pCold-DDX6

A DNA fragment coding DDX43 or DDX6 was amplified by PCR and cloned into pCold-I vector (Takara) by In-fusion cloning kit (Takara).

pFastBac-6HFLAGSBP-Spn-E-WT, E251Q

A DNA fragment coding Spn-E-WT or E251Q was amplified by PCR and subcloned into pcDNA5/FRT/TO vector (Thermo Fisher Scientific) inserted a FLAGSBP sequence. Then, a DNA fragment coding 6HisFLAGSBP-Spn-E-WT, E251Q was amplified by PCR and cloned into pFastBac vector (Thermo Fisher Scientific) by In-fusion cloning kit (Takara).

pIEx4-piR484-A reporter

Synthesized DNA oligos that have chimeric target sequence of piR484 and piR2986 were annealed (see Fig EV3A) and inserted into the BamHI and HindIII sites of pIEx4 vector (Merck Millipore/Novagen).

pIB-piggyBac piRNA reporter

piggyBac piRNA target site was inserted into the middle of the V5 coding sequence in pIB-V5/His vector (Thermo Fisher Scientific) by site-directed mutagenesis. For linearization, the plasmid was digested with *AgeI*, which cleaves 20 bp downstream of

the *piggyBac* piRNA target site (see Fig 3C).

The primer sequences for plasmid construction are listed in Table EV1.

Antibodies and western blotting

Rabbit anti-Siwi, anti-BmAgo3, anti-Spn-E, and biotinylated BmAgo3 antibodies were described previously (Izumi et al. 2020,2022). Rabbit anti-DDX6 antibody was generated by immunizing N-terminally His-tagged full-length DDX6. Anti-FLAG (M2, Merck Millipore/Sigma), anti-DYKDDDDK peroxidase conjugated (Wako), anti-HA (3F10, Merck Millipore/Roche), anti-α-Tubulin (B-5-1-2, Merck Millipore/Sigma) antibodies were purchased. Chemiluminescence was induced by Luminata Forte Western HRP Substrate (Merck Millipore) and images were acquired by Amersham Imager 600 (Cytiva).

Immunoprecipitation

For BmAgo3 immunoprecipitation, cells were resuspended in buffer A [25 mM Tris-HCl (pH 7.6), 150 mM NaCl, 1.5 mM $MgCl_2$, 0.2% sodium deoxycholate, 0.1% lithium dodecyl sulfate, 0.4% NP-40, 0.5 mM DTT, 1 × Complete EDTA-free protease inhibitor (Merck Millipore/Roche), 1 × PhosSTOP (Merck Millipore/Roche)] and incubated on ice for 20 min. The cell suspension was centrifuged at 17,000 × g for 30 min at 4°C, and the cleared lysate was diluted with an equal volume of buffer A without detergents. The cell lysate was incubated with normal rabbit IgG (Cell signaling) or anti-BmAgo3 antibody at 4°C for 1 h, and then Dynabeads Protein G (Thermo Fisher Scientific/Invitrogen) was added. After incubation at 4°C for 1.5 h, the beads were washed with buffer A without protease inhibitors and phosphatase inhibitors five times,

and the immunopurified complex was eluted with SDS sample buffer. For FLAG-Spn-E immunoprecipitation, cells were resuspended in buffer B [25 mM Tris-HCl (pH 7.6), 150 mM NaCl, 1.5 mM $MgCl_2$, 0.25% Triton X-100, 0.5 mM DTT, 1 × Complete EDTA-free protease inhibitor (Merck Millipore/Roche), 1 × PhosSTOP (Merck Millipore/Roche)] and homogenized with a Dounce homogenizer on ice. The cell lysate was centrifuged at 17,000 × g for 30 min at 4°C, and the supernatant was incubated with Dynabeads Protein G (Thermo Fisher Scientific/Invitrogen) pre-conjugated with anti-FLAG antibody (M2, Merck Millipore/Sigma) at 4°C for 1.5 h. The beads were washed with buffer C [25 mM Tris-HCl (pH 7.4), 150 mM NaCl, 1.5 mM $MgCl_2$, 0.5% Triton X-100, 0.5 mM DTT] five times, and the immunopurified complexes were eluted with 3X FLAG peptide (Merck Millipore/Sigma). For tandem IP experiment, the eluate was diluted with an equal volume of buffer D [30 mM Hepes-KOH (pH 7.4), 100 mM KOAc, 2 mM $Mg(OAc)_2$, 0.5 mM DTT]. One third of the lysate was incubated with normal rabbit IgG (Cell signaling) and the remaining was incubated with anti-BmAgo3 antibody at 4°C for 30 min, and then Dynabeads Protein G (Thermo Fisher Scientific/Invitrogen) was added. After incubation at 4°C for 1.5 h, the beads were washed with buffer C five times. The BmAgo3 immunoprecipitated beads were divided into two and incubated in buffer D with/without 200 μg/ml RNase A (Qiagen) at 30°C for 15 min. The beads were washed with buffer D twice and the immunopurified complex was eluted with SDS sample buffer. For Siwi immunoprecipitation in artificial piRNA reporter experiments, cells were resuspended in buffer B and homogenized with a Dounce homogenizer on ice. The cell lysate was centrifuged at 17,000 × g for 30 min at 4°C. The supernatant further supplemented with Triton X-100 (final concentration, 1%) was incubated with anti-Siwi antibody at 4°C for 1 h, and then Dynabeads Protein

G (Thermo Fisher Scientific/Invitrogen) was added. After incubation at 4°C for 1.5 h, the beads were washed with buffer E [25 mM Tris-HCl (pH 7.4), 150 mM NaCl, 1.5 mM $MgCl_2$, 1% Triton X-100, 0.5 mM DTT] five times. A portion of the immunopurified complexes was eluted with SDS sample buffer, and the remainder was eluted with TRI Reagent (Molecular Research Center) for northern blot analysis.

Purification of recombinant proteins

pCold-DDX43 and pCold-DDX6 were transformed into Rosetta 2 (DE3) competent cells (Merck Millipore/Novagen). The cells were cultured at 37°C until the OD_{600} reached ~0.6, and then cooled on ice for 30 min. Protein expression was induced with 1 mM IPTG at 15°C for overnight. The cell pellets were resuspended in His purification buffer [50 mM Hepes-KOH (pH 7.4), 300 mM NaCl, 13 mM imidazole, 0.2 mM TECP, 10 μg/ml leupeptin, 10 μg/ml aprotinin, 1 μg/ml pepstatin A, 1 × Complete EDTA-free protease inhibitor cocktail (Merck Millipore/Roche)] and sonicated with Bioruptor II (CosmoBio). The cell lysate was centrifuged at 17,000 × g at 4°C for 20 min. The cleared lysate was added to cOmplete His-Tag Purification Resin (Merck Millipore/Roche) and incubated at 4°C for 1.5 h. After washing the resin with the His purification buffer, the bound proteins were eluted with elution buffer [50 mM Hepes-KOH (pH 7.4), 150 mM NaCl, 300 mM imidazole, 0.2 mM TECP]. Peak fractions were pooled and dialyzed with PBS overnight. 6HisFLAGSBP-Spn-E (WT or E251Q) was expressed in SF9 cells by the Bac-to-Bac Baculovirus Expression system (Thermo Fisher Scientific/Invitrogen). The SF9 cells were resuspended in buffer F [25 mM Tris-HCl (pH 7.4), 150 mM NaCl, 1.5 mM $MgCl_2$, 0.5% Triton X-100, 0.4% NP-40, 1 mM DTT, 1 × Complete EDTA-free protease inhibitor (Merck Millipore/Roche), 1 ×

PhosSTOP (Merck Millipore/Roche)] and homogenized with a Dounce homogenizer. The cell homogenate was centrifuged at 17,000 × g for 30 min at 4°C. The supernatant supplemented with Triton X-100 (1%, final concentration), NaCl (450 mM, final concentration), and RNaseA (150 μg/ml, final concentration, Qiagen) was incubated with Streptavidin Sepharose High Performance (Cytiva) at 4°C for 2 h. The Sepharose beads were washed with buffer G [25 mM Tris-HCl (pH 7.4), 550 mM NaCl, 1.5 mM $MgCl_2$, 1% Triton X-100, 0.4% NP-40, 1 mM DTT], and rinsed with buffer H [25 mM Tris-HCl (pH 7.4), 150 mM NaCl, 1.5 mM $MgCl_2$, 0.05% Triton X-100, 1 mM DTT]. 6HisFLAGSBP-Spn-E (WT or E251Q) proteins were eluted with buffer H containing 2.5 mM Biotin, and the eluate was dialyzed with PBS overnight.

In vitro cleavage fragment release assay

To generate 5' and internally radiolabeled target RNAs, synthesized 5' and 3' fragments of the target RNA were ^{32}P-radiolabeled at the 5' end using T4 polynucleotide kinase (Takara). After gel purification, the radiolabeled 5' fragment was ligated to a 5'-phosphorylated unlabeled 3' fragment, and the radiolabeled 3' fragment was ligated to an unlabeled 5' fragment by splinted ligation with T4 DNA ligase (NEB) at 30°C for 2 h, respectively. The radiolabeled target RNA was gel-purified and used for the assay. BmAgo3 immunoprecipitation for the cleavage assay was described previously (Izumi *et al*, 2022). Target cleavage assay was performed at 40°C for 2 h in a 10 μl reaction containing 3 μl of 40 × reaction mix (Haley *et al*, 2003), and 2 nM ^{32}P- radiolabeled target RNA. After the supernatant was removed, BmAgo3-bound beads were further incubated in buffer D containing 5 mM ATP, 350 nM recombinant proteins at 30°C for 1 h. Then, the supernatant and bead fractions were treated separately with proteinase K,

and the target RNA was purified by EtOH precipitation. An image of the target RNA, separated on an 8% denaturing polyacrylamide gel, was captured using the FLA-7000 imaging system (Fujifilm Life Sciences). Oligonucleotides used for target RNA preparation were listed in Table EV1.

RNA extraction, northern blotting, and quantitative real-time PCR

For real-time PCR, northern blotting, and preparation of small RNA libraries, total RNA was prepared using TRI Reagent (Molecular Research Center) or mirVana miRNA Isolation Kit (Thermo Fisher Scientific/Invitrogen). Northern blotting and quantitative real-time PCR were performed as described previously (Izumi *et al*, 2020). The probes for northern blotting and the primer sequences for real-time PCR are listed in Table EV1.

Immunofluorescence

BmN4 cells were fixed with 4% paraformaldehyde in PBS at room temperature for 10 min, then the cells were permeabilized with 0.3% Triton X-100 in PBS for 5 min. After pre-incubation with blocking buffer [PBS supplemented with 1% BSA (Merck Millipore/Sigma) and 0.1% Triton X-100] at room temperature for 1 h, the cells were incubated with primary antibodies [anti-FLAG antibody (M2, Merck Millipore/Sigma, 1/300), anti-HA antibody (3F10, Merck Millipore/Roche, 1/300), anti-Siwi antibody (1/400), anti-BmAgo3 antibody (1/300), anti-Spn-E antibody (1/250), anti-DDX6 antibody (1/250)] in blocking buffer at 4 °C overnight. Alexa Fluor 488 donkey anti-mouse IgG, Alexa Fluor 488 donkey anti-rat IgG, Alexa Fluor 647 donkey anti-rabbit IgG, and Alexa Fluor 647 goat anti-rat IgG secondary antibodies (Thermo Fisher

Scientific) were used for detection. Biotinylated anti-BmAgo3 antibody was probed after incubation with the secondary antibody, and the BmAgo3 signal was detected by Cy3-Streptavidin (Jackson ImmunoResearch). Images were captured using Olympus FV3000 confocal laser scanning system with a × 60 oil immersion objective lens (PLAPON 60XO, NA 1.42, Olympus) and processed FV31S-SW Viewer software and Adobe Photoshop Elements 10.

Mass spectrometry analysis

Immunoprecipitated BmAgo3 complexes separated by SDS-PAGE were stained with coomassie brilliant blue (CBB), and the p160 band was excised from the gel, followed by in-gel digestion with trypsin (Promega) at 37°C for overnight. LC-MS/MS analysis was conducted by LTQ-Orbitrap Velos mass spectrometer (Thermo Fisher Scientific) equipped with a nanoLC interface (Zaplous Advance nanoUHPLC HTS-PAL xt System) (AMR). The nanoLC gradient was delivered at 500 nL/min and consisted of a linear gradient of mobile phase developed from 5 to 45% of acetonitrile in 60-180 min. Proteins were identified by the search algorithms Proteome Discoverer 2.4 (Thermo Fisher Scientific) using the protein database of *Bombyx mori* from NCBI.

Small RNA library preparation

Small RNA libraries were constructed from 20−50 nt total RNAs according to the Zamore lab's open protocol (https://www.dropbox.com/s/r5d7aj3hhyaborq/) with some modifications (Fu *et al*, 2018). The 3′ adapter was conjugated with an amino CA linker instead of dCC at the 3′ end (GeneDesign) and adenylated using 5′ DNA adenylation kit at the 5′ end (NEB). To reduce a ligation bias, four random nucleotides were included in

the 3′ and 5′ adapters [(5′-rAppNNNNTGGAATTCTCGGGTGCCAAGG/amino CA linker-3′) and (5′-GUUCAGAGUUCUACAGUCCGACGAUCNNNN-3′)] and the adapter ligation was performed in the presence of 20% PEG-8000. After the 3′ adapter ligation at 16 °C for ≥16 h, RNAs were size-selected by urea PAGE. For RNA extraction from a polyacrylamide gel, ZR small-RNA PAGE Recovery Kit (ZYMO Research) was used. Small RNA libraries were sequenced on a HiSeq 4000 or DNBSEQ-G400 platform.

Sequence analysis of small RNA libraries

First, the adapter was removed by cutadapt using the sequence of the common part of the 3' adapter sequence after NNNN (Martin, 2011). The sequences were then converted to fasta using fastq_to_fasta in the FASTX-Toolkit, and the completely duplicated sequences were removed using fastx_collapser to thin out to one (FASTX-Toolkit; http://hannonlab.cshl.edu/fastx_toolkit/). Finally, cutadapt was used to remove 4 nts of the UMI sequences from the 5' and 3' ends, respectively. Final sequences longer than 12 nt were used for analysis. Libraries were normalized by the number of reads that mapped to the genome allowing a single nucleotide mismatch by bowtie.

Mapping to transposons was done using bowtie, allowing for a single nucleotide mismatch (Langmead *et al,* 2009). Sam files were converted to bam files by SAMtools (Li *et al,* 2009) and then to bed files by BEDTools (Quinlan & Hall, 2010). Among the mapped reads, reads between 23 and 32 nts in length were extracted as piRNAs using the awk command in Linux. The number of reads mapped to each transposon was measured using coverageBed in BEDtools, and the results were read into R to create a MAplot (Quinlan & Hall, 2010).

For individual piRNAs, mapping was performed with bowtie, allowing single nucleotide mismatches and multi-mapping to the surrounding regions of 3,236 previously constructed piRNA sequences (Izumi *et al*, 2016). Sam files were converted to bam files by SAMtools (Li *et al*, 2009) and then to bed files by BEDTools (Quinlan & Hall, 2010). Among the mapped reads, reads between 23 and 32 nts were extracted as piRNAs using the awk command in Linux. The results were used to obtain the position of the 5' end of the nearby piRNA for each piRNA using a custom script in R for subsequent analysis. Of the 3,236 piRNAs, 352 derived from TE1_bm_1645_LINE/R4, a transposon containing rRNA, were excluded from the analysis.

Definition of S→A, A→S, and S→S piRNAs

Only small RNA reads with 5'-end matches to the previously defined 3,236 piRNAs were extracted from the Siwi-IP and BmAgo3-IP libraries, and the IP libraries were normalized by the total read count of the 3,236 piRNAs. Based on the RPM values, these piRNAs were then classified into Siwi-bound piRNAs and BmAgo3-bound piRNAs (i.e. “S” or “A” after the arrow) depending on whether they were more abundant in the Siwi-IP or the BmAgo3-IP library. Next, a similar analysis was performed on piRNAs with 5' 10-nt overlapping sequences to determine whether the ping-ping partner was Siwi or BmAgo3 (i.e. “S” or “A” before the arrow) based on their abundance in the IP libraries. The 352 rRNA-derived piRNAs, 212 piRNAs for which the binding PIWI protein of 5' 10-nt complementary piRNAs could not be determined (including many piRNAs that had no more than 1 read in the IP libraries), and 32 BmAgo3-bound piRNAs abundant in both sense and antisense strands were excluded. Finally, 571 S→S piRNAs, 1,036 A→S piRNAs, and 1,033 S→A piRNAs were used

for analysis.

Data availability

The sequencing data is deposited at the DDBJ database (https://www.ddbj.nig.ac.jp) under accession number DRA017492–DRA017493.

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Author Contributions

N.I., K.S. and Y.T. conceived and designed the experiments and wrote the manuscript. N.I. performed biochemical and cell biological experiments. K.S. performed bioinformatics analyses. L.N. performed mass spectrometry analysis. Y.T. supervised the research. All the authors discussed the results and approved the manuscript.

Conflict of interest

The authors declare that they have no conflict of interest.

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Figure Legends

Fig 1. The ATPase deficient Spn-E-EQ forms aggregates with BmAgo3.

A CBB staining of immunoprecipitated BmAgo3 complexes from BmN4 cells treated with dsRNA targeting *Rluc* or *Siwi*. *Rluc*; *Renilla luciferase,* control. HC; IgG heavy chain, LC; IgG light chain.

B Subcellular localization of BmAgo3, Spn-E, and FLAG-DDX43 in BmN4 cells treated with dsRNA targeting *Rluc* or *Siwi*. *Rluc*; *Renilla luciferase,* control. Scale bar, 5

μm.

C Subcellular localization of FLAG-Spn-E (wild type or EQ) and BmAgo3 in BmN4 cells treated with dsRNA targeting the *Spn-E* 3' UTR. Scale bar, 5 μm.

D Western blot analysis of immunopurified FLAG-Spn-E (wild type or EQ) complexes from BmN4 cells treated with dsRNA targeting the *Spn-E* 3' UTR.

E Northern blot analysis of piR1712, piR2986, and piR484 in BmN4 cells co-transfected with FLAG-Spn-E (wild type or EQ) plasmid and dsRNA targeting the *Spn-E* 3' UTR.

Fig 2. Depletion of Spn-E decreases BmAgo3-dependent production of Siwi-bound piRNAs while increasing Siwi-Siwi homotypic ping-pong.

A MA plot showing piRNA expression changes between control KD (*Rluc* RNAi) and *Spn-E* KD using dsRNA targeting the *Spn-E* 3' UTR. Each dot represents one piRNA. Based on the expression change, piRNAs were divided into three groups; "increased" (red, n = 825), "unchanged" (green, n = 824), and "decreased" (blue, n = 825).

B Relative fractions of 1U10A, 1U but not 10A, 10A but not 1U, and neither 1U nor 10A piRNAs of each group defined in (A).

C Schematic representation of A→S, S→A, and S→S piRNAs.

D Expression changes of A→S, S→A, and S→S piRNAs in *Spn-E* KD relative to control KD (*Rluc* RNAi). Two different dsRNAs targeting the *Spn-E* CDS and 3' UTR were used.

E Expression changes of A→S, S→A, and S→S piRNAs in the indicated conditions relative to control KD (*Rluc* RNAi). The data of *Spn-E* RNAi (UTR) in (D)

is included for comparison.

F Summary of the results from the *Spn-E* KD rescue experiment. *Spn-E* KD decreases A→S piRNAs and increases S→S piRNAs. A→S piRNA production requires the ATPase activity of Spn-E, whereas the suppression of S→S piRNA production does not.

Fig 3. Artificial Siwi-bound piRNA production is impaired by Spn-E KD but not by DDX43 KD.

A Schematic representation of the piR484-A reporter. piR484-A is an artificial A→S piRNA with a chimera sequence of piR484 and piR2986. Details are shown in Fig EV3A.

B Siwi was immunoprecipitated from BmN4 cells co-transfected with piR484-A reporter plasmid and dsRNA targeting indicated genes for RNAi. Immunoprecipitated Siwi and Siwi-bound piR484-A were detected by western blotting and northern blotting, respectively. *Rluc*; *Renilla luciferase,* control.

C Schematic representation of the production of *piggyBac* piRNA reporter-derived artificial Siwi-bound piRNA. (Left) The circular plasmid produces a reporter RNA with a long 3' region. After cleavage by *piggyBac* piRNA-loaded BmAgo3, the 3' end of Siwi-loaded reporter RNA is processed by an unknown downstream cleavage event and/or trimming by Trimmer. (Right) After cleavage by *piggyBac* piRNA-loaded BmAgo3, the reporter RNA from the linearized plasmid is expected to be 30 nt long, which is similar in length to endogenous piRNAs. Consequently, additional 3' end processing is unnecessary in theory.

D Siwi was immunoprecipitated from BmN4 cells co-transfected with circular or

linearized *piggyBac* piRNA reporter plasmid and dsRNA targeting indicated genes for RNAi. Immunoprecipitated Siwi and reporter-derived artificial Siwi-bound piRNA (art-Siwi piRNA) were detected by western blotting and northern blotting, respectively. *Rluc*; *Renilla luciferase,* control.

E KD rescue experiment of Spn-E using *piggyBac* piRNA reporter. Siwi was immunoprecipitated from BmN4 cells co-transfected with circular *piggyBac* piRNA reporter plasmid, FLAG-Spn-E expression plasmid, and dsRNA targeting the *Spn-E* 3' UTR. Immunoprecipitated Siwi and reporter-derived artificial Siwi-bound piRNA (art-Siwi piRNA) were detected by western blotting and northern blotting, respectively. *Rluc*; *Renilla luciferase,* control.

Expanded View Figure Legends

Fig EV1. Characterization of Spn-E-EQ aggregates and BmAgo3 cleavage fragment release assay.

A Western blot analysis of whole cell lysate of BmN4 cells treated with dsRNA for *Rluc* (control) or *DDX6*. The anti-DDX6 antibody successfully detects endogenous DDX6.

B Subcellular localization of FLAG-Spn-E-EQ, DDX6, a P-body marker protein, and BmAgo3 in BmN4 cells. Scale bar, 5 μm.

C Subcellular localization of FLAG-Spn-E-EQ, BmAgo3 and Siwi in BmN4 cells. Scale bar, 5 μm.

D Tandem IP experiment on BmN4 cells co-transfected with FLAG-Spn-E-EQ

expression plasmid and dsRNA targeting the *Spn-E* 3' UTR. FLAG-Spn-E-EQ was first immunopurified with FLAG tag, and the resulting immunopurified complex was then subjected to a second IP with normal rabbit IgG (Contl-IgG) or anti-BmAgo3 antibody. Siwi in the second immunoprecipitates was detected by western blotting with or without RNase A treatment.

E CBB staining of purified recombinant Spn-E and DDX43 proteins (rSpn-E and rDDX43) used for in vitro cleavage fragment release assay.

F (Top) Schematic explanation of the in vitro cleavage fragment release assay. To detect cleaved 5' and 3' fragments separately, target RNA was radiolabeled at different positions (*). The 5' or internally radiolabeled target RNAs were subjected to the cleavage assay using BmAgo3 immunoprecipitates. After the reaction, the bead fraction was incubated with rSpn-E or rDDX43 in the presence of ATP. (Bottom) The cleaved fragments in the supernatant and bead fractions were detected by autoradiography.

G Subcellular localization of FLAG-DDX43 (wild type or DA, an ATPase-deficient mutant) and BmAgo3 in BmN4 cells. Scale bar, 5 μm.

H Subcellular localization of FLAG-Spn-E-EQ, HA-DDX43, and BmAgo3 in BmN4 cells. Scale bar, 5 μm.

Fig EV2. Expression changes of TE-mapped piRNAs upon KD of *Spn-E* or *DDX43*.

A Western blot analysis of whole cell lysate from BmN4 cells treated with dsRNA for *Rluc* (control), *Spn-E*, or *DDX43*. Two different dsRNAs (*Spn-E*: CDS and 3' UTR, *DDX43*: two different regions of CDS, #1 and #2) were used for RNAi. *Rluc*; *Renilla luciferase.*

B Quantitative real-time PCR analysis of the expression of *DDX43* in BmN4 cells

treated with dsRNA for *Rluc* (control), *Spn-E*, or *DDX43*. Relative mRNA expression levels normalized to that of *rp49* are shown. *Rluc*; *Renilla luciferase*.

C MA plots showing piRNA expression changes for each TE between control KD (*Rluc* RNAi) and *Spn-E* or *DDX43* KD. Two different dsRNAs (CDS and 3' UTR) were used for *Spn-E* RNAi. Each dot represents one TE. TEs with increased piRNA production in *Spn-E* RNAi (UTR) are colored red.

D MA plot showing piRNA expression changes between control KD (*Rluc* RNAi) and *Spn-E* KD using dsRNA targeting the *Spn-E* CDS. Each dot represents one piRNA. Based on the three groups defined in Fig 2A, piRNAs were color-coded: "increased" (red, n = 825), "unchanged" (green, n = 824), and "decreased" (blue, n = 825).

E MA plot showing piRNA expression changes between control KD (*Rluc* RNAi) and *Spn-E* KD using dsRNA targeting the *Spn-E* CDS. Each dot represents one piRNA. Based on the expression change, piRNAs were divided into three groups; "increased" (red, n = 805), "unchanged" (green, n = 805), and "decreased" (blue, n = 805).

F Relative fractions of 1U10A, 1U but not 10A, 10A but not 1U, and neither 1U nor 10A piRNAs of each group in (E).

G Scatter plots showing PIWI binding bias of 1U but not 10A, 10A but not 1U, and 1U10A piRNAs (x-axis) and that of their putative partner piRNAs in the ping-pong cycle (y-axis).

H Expression changes of A→S, S→A, and S→S piRNAs in *DDX43* KD relative to control KD (*Rluc* RNAi). Two different dsRNAs targeting *DDX43* CDS were used for RNAi. *Rluc*; *Renilla luciferase.*

Fig EV3. Construction of the piR484-A reporter system and Spn-E KD rescue experiment using the piR484-A reporter.

A Schematic explanation of the construction of piR484-A reporter. piR484 is an S→A piRNA, and the sequence including the 5' 10 nt and the upstream region of piR484 was replaced with the corresponding region of piR2986, an A→S piRNA, resulting in an artificial A→S piRNA, piR484-A. The downstream sequence of piR484 that contains a Siwi-bound piRNA target sequence was used without modification.

B Quantitative real-time PCR analysis of the expression of *DDX43* in the reporter experiments in Fig 3B and 3D. Relative mRNA expression levels normalized to that of *rp49* are shown. *Rluc*; *Renilla luciferase,* control.

C KD rescue experiment of Spn-E using the piR484-A reporter. Siwi was immunoprecipitated from BmN4 cells co-transfected with piR484-A reporter plasmid, FLAG-Spn-E expression plasmid, and dsRNA targeting the *Spn-E* 3' UTR. Immunoprecipitated Siwi and Siwi-bound piR484-A were detected by western blotting and northern blotting, respectively. *Rluc*; *Renilla luciferase,* control.

Figure 1

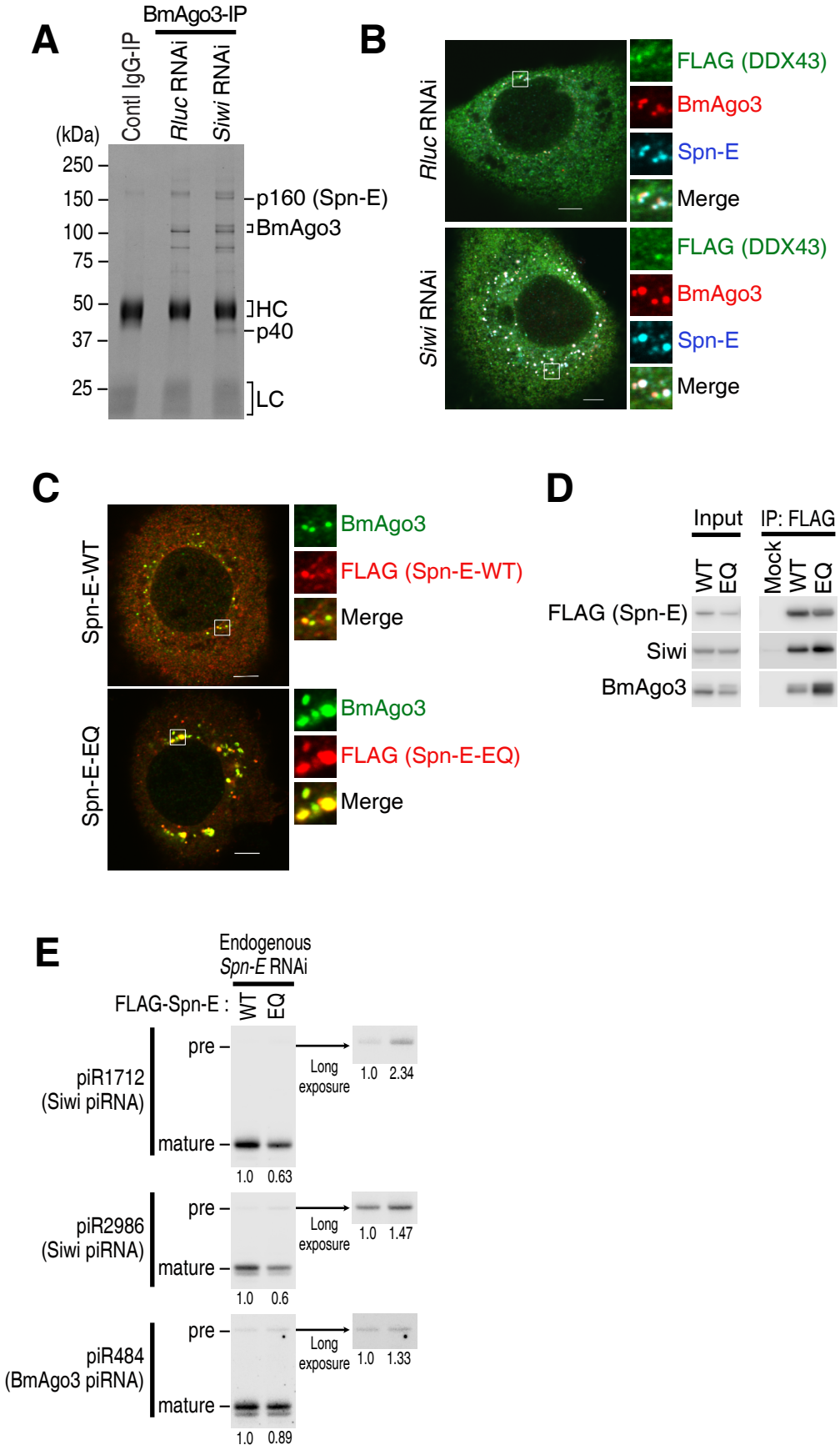

A
BmAgo3-IP
Contl IgG-IP
Rluc RNAi
Siwi RNAi
(kDa)
250
150
100
75
50
37
25
p160 (Spn-E)
BmAgo3
HC
p40
LC
B
Rluc RNAi
Siwi RNAi
FLAG (DDX43)
BmAgo3
Spn-E
Merge
C
Spn-E-WT
Spn-E-EQ
BmAgo3
FLAG (Spn-E-WT)
FLAG (Spn-E-EQ)
Merge
D
Input
IP: FLAG
WT
EQ
Mock
FLAG (Spn-E)
Siwi
BmAgo3
E
Endogenous
Spn-E RNAi
FLAG-Spn-E :
WT
EQ
piR1712
(Siwi piRNA)
pre
mature
Long exposure
1.0
2.34
1.0
0.63
piR2986
(Siwi piRNA)
1.0
1.47
1.0
0.6
piR484
(BmAgo3 piRNA)
1.0
1.33
1.0
0.89

Figure 2

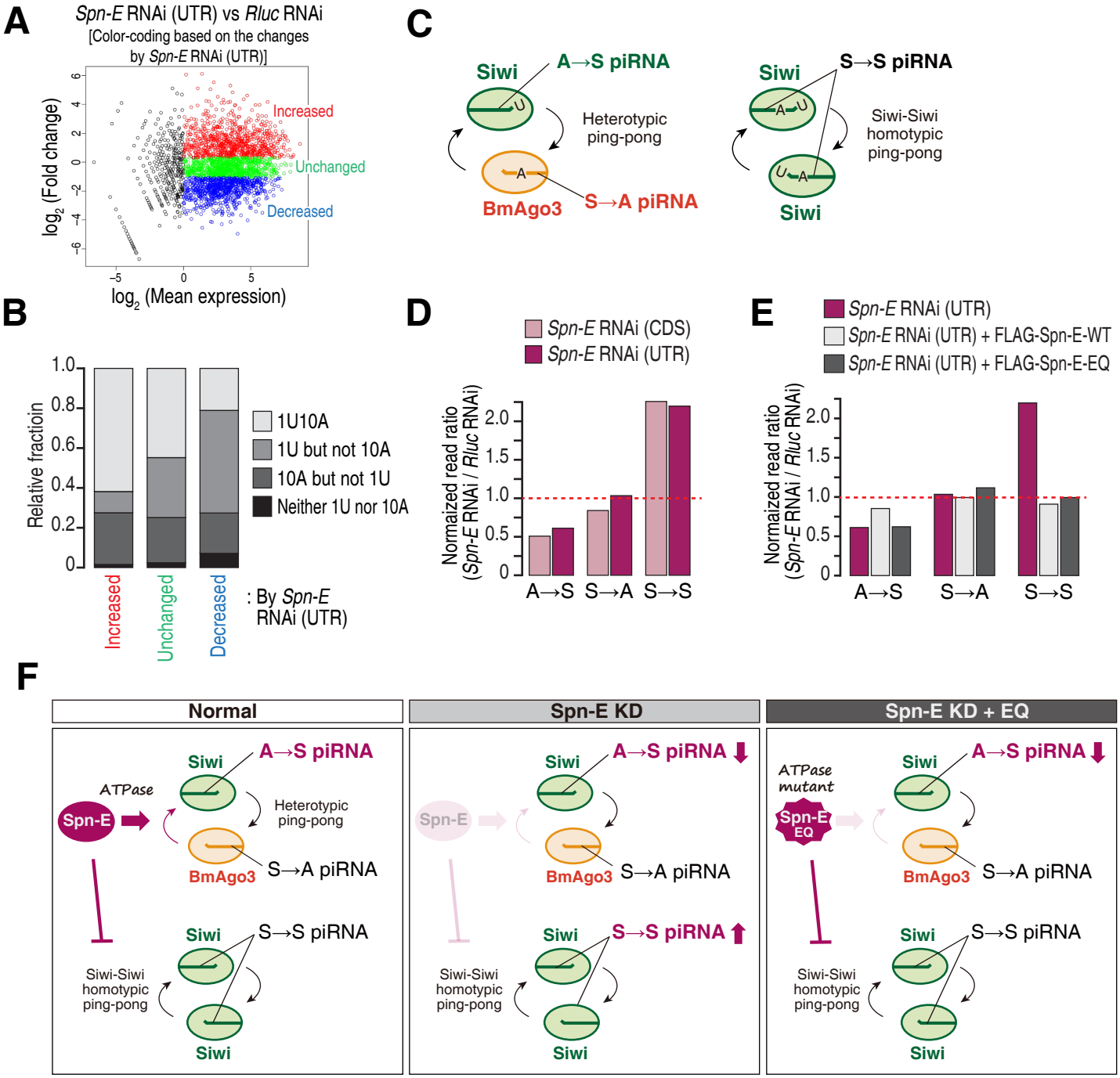

A
Spn-E RNAi (UTR) vs Rluc RNAi
[Color-coding based on the changes by Spn-E RNAi (UTR)]
Increased
Unchanged
Decreased
log2 (Fold change)
log2 (Mean expression)
B
Relative fractioin
1U10A
1U but not 10A
10A but not 1U
Neither 1U nor 10A
Increased
Unchanged
Decreased
: By Spn-E RNAi (UTR)
C
Siwi
A→S piRNA
Heterotypic ping-pong
BmAgo3
S→A piRNA
Siwi
S→S piRNA
Siwi-Siwi homotypic ping-pong
Siwi
D
Spn-E RNAi (CDS)
Spn-E RNAi (UTR)
Normaized read ratio (Spn-E RNAi / Rluc RNAi)
A→S
S→A
S→S
E
Spn-E RNAi (UTR)
Spn-E RNAi (UTR) + FLAG-Spn-E-WT
Spn-E RNAi (UTR) + FLAG-Spn-E-EQ
Normaized read ratio (Spn-E RNAi / Rluc RNAi)
A→S
S→A
S→S
F
Normal
Spn-E KD
Spn-E KD + EQ
ATPase
Spn-E
Siwi
A→S piRNA
Heterotypic ping-pong
BmAgo3
S→A piRNA
S→S piRNA
Siwi-Siwi homotypic ping-pong
Siwi
A→S piRNA ⬇
S→S piRNA ⬆
ATPase mutant
Spn-E EQ

Figure 3

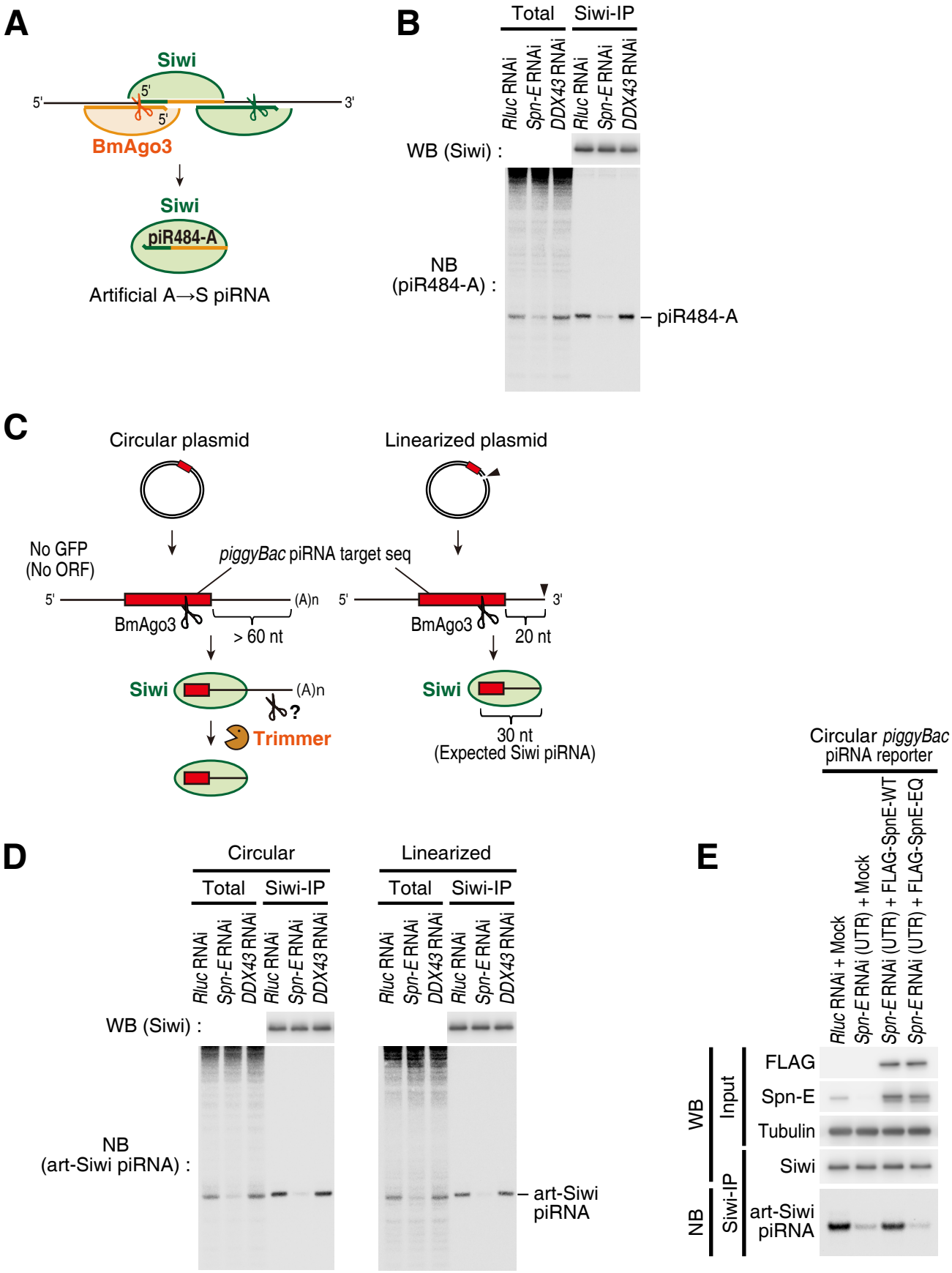

A
Siwi
5'
3'
5'
5'
BmAgo3
Siwi
piR484-A
Artificial A→S piRNA
B
Total
Siwi-IP
Rluc RNAi
Spn-E RNAi
DDX43 RNAi
Rluc RNAi
Spn-E RNAi
DDX43 RNAi
WB (Siwi) :
NB
(piR484-A) :
piR484-A
C
Circular plasmid
Linearized plasmid
No GFP
(No ORF)
piggyBac piRNA target seq
5'
(A)n
BmAgo3
> 60 nt
5'
3'
BmAgo3
20 nt
Siwi
(A)n
?
Trimmer
Siwi
30 nt
(Expected Siwi piRNA)
D
Circular
Linearized
Total
Siwi-IP
Total
Siwi-IP
Rluc RNAi
Spn-E RNAi
DDX43 RNAi
Rluc RNAi
Spn-E RNAi
DDX43 RNAi
Rluc RNAi
Spn-E RNAi
DDX43 RNAi
Rluc RNAi
Spn-E RNAi
DDX43 RNAi
WB (Siwi) :
NB
(art-Siwi piRNA) :
art-Siwi
piRNA
E
Circular piggyBac
piRNA reporter
Rluc RNAi + Mock
Spn-E RNAi (UTR) + Mock
Spn-E RNAi (UTR) + FLAG-SpnE-WT
Spn-E RNAi (UTR) + FLAG-SpnE-EQ
WB
Input
FLAG
Spn-E
Tubulin
Siwi
NB
Siwi-IP
art-Siwi
piRNA

Figure EV1

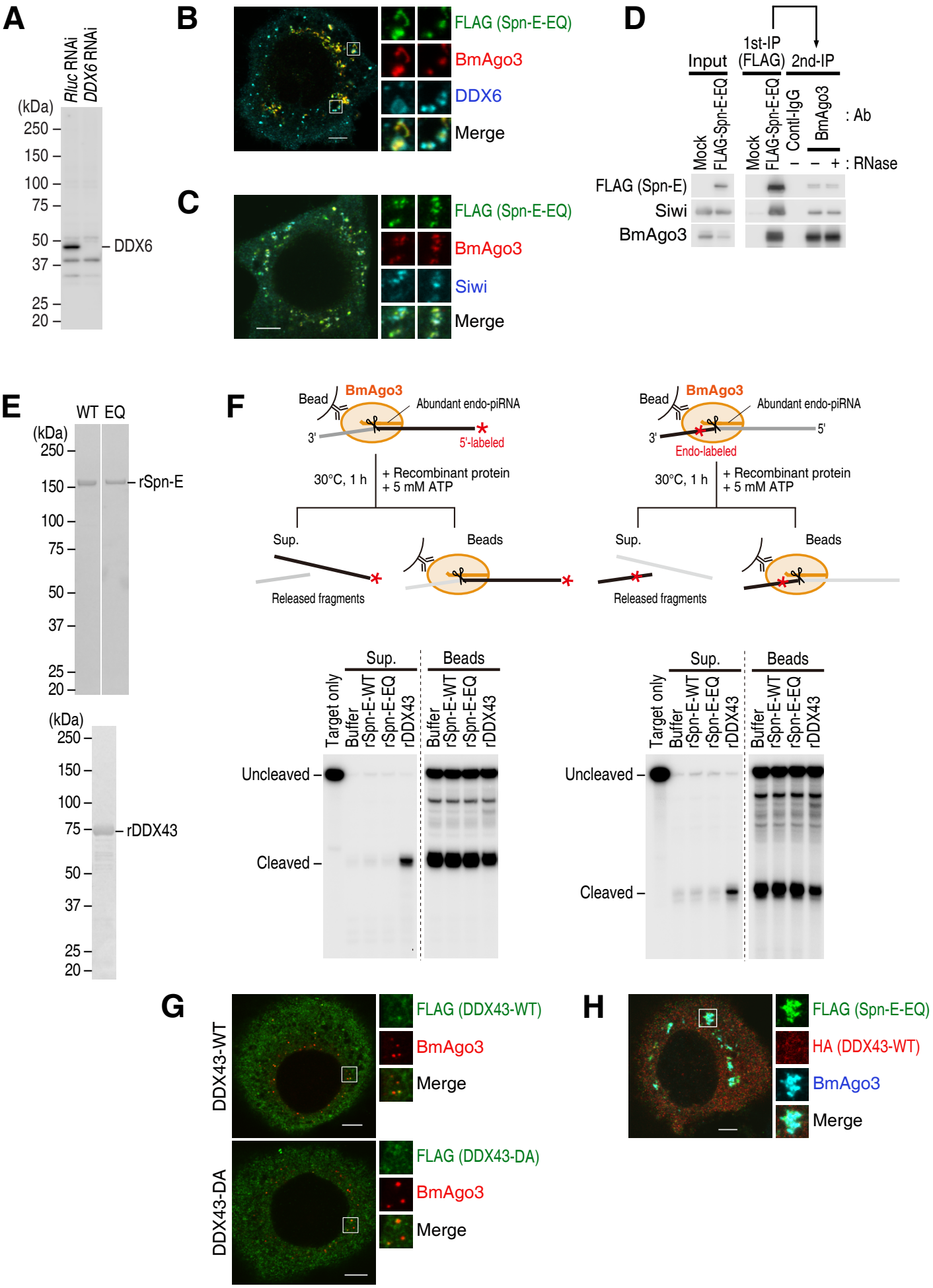

A
Rluc RNAi
DDX6 RNAi
(kDa)
250
150
100
75
50
37
25
20
DDX6
B
FLAG (Spn-E-EQ)
BmAgo3
DDX6
Merge
C
FLAG (Spn-E-EQ)
BmAgo3
Siwi
Merge
D
Input
1st-IP (FLAG)
2nd-IP
Mock
FLAG-Spn-E-EQ
Mock
FLAG-Spn-E-EQ
Contl-IgG
BmAgo3
: Ab
–
–
+
: RNase
FLAG (Spn-E)
Siwi
BmAgo3
E
WT
EQ
(kDa)
250
150
100
75
50
37
25
20
rSpn-E
(kDa)
250
150
100
75
50
37
25
20
rDDX43
F
Bead
BmAgo3
Abundant endo-piRNA
3'
5'-labeled
30°C, 1 h
+ Recombinant protein
+ 5 mM ATP
Sup.
Beads
Released fragments
Bead
BmAgo3
Abundant endo-piRNA
3'
5'
Endo-labeled
30°C, 1 h
+ Recombinant protein
+ 5 mM ATP
Sup.
Beads
Released fragments
Sup.
Beads
Target only
Buffer
rSpn-E-WT
rSpn-E-EQ
rDDX43
Buffer
rSpn-E-WT
rSpn-E-EQ
rDDX43
Uncleaved
Cleaved
Sup.
Beads
Target only
Buffer
rSpn-E-WT
rSpn-E-EQ
rDDX43
Buffer
rSpn-E-WT
rSpn-E-EQ
rDDX43
Uncleaved
Cleaved
G
DDX43-WT
FLAG (DDX43-WT)
BmAgo3
Merge
DDX43-DA
FLAG (DDX43-DA)
BmAgo3
Merge
H
FLAG (Spn-E-EQ)
HA (DDX43-WT)
BmAgo3
Merge

Figure EV2

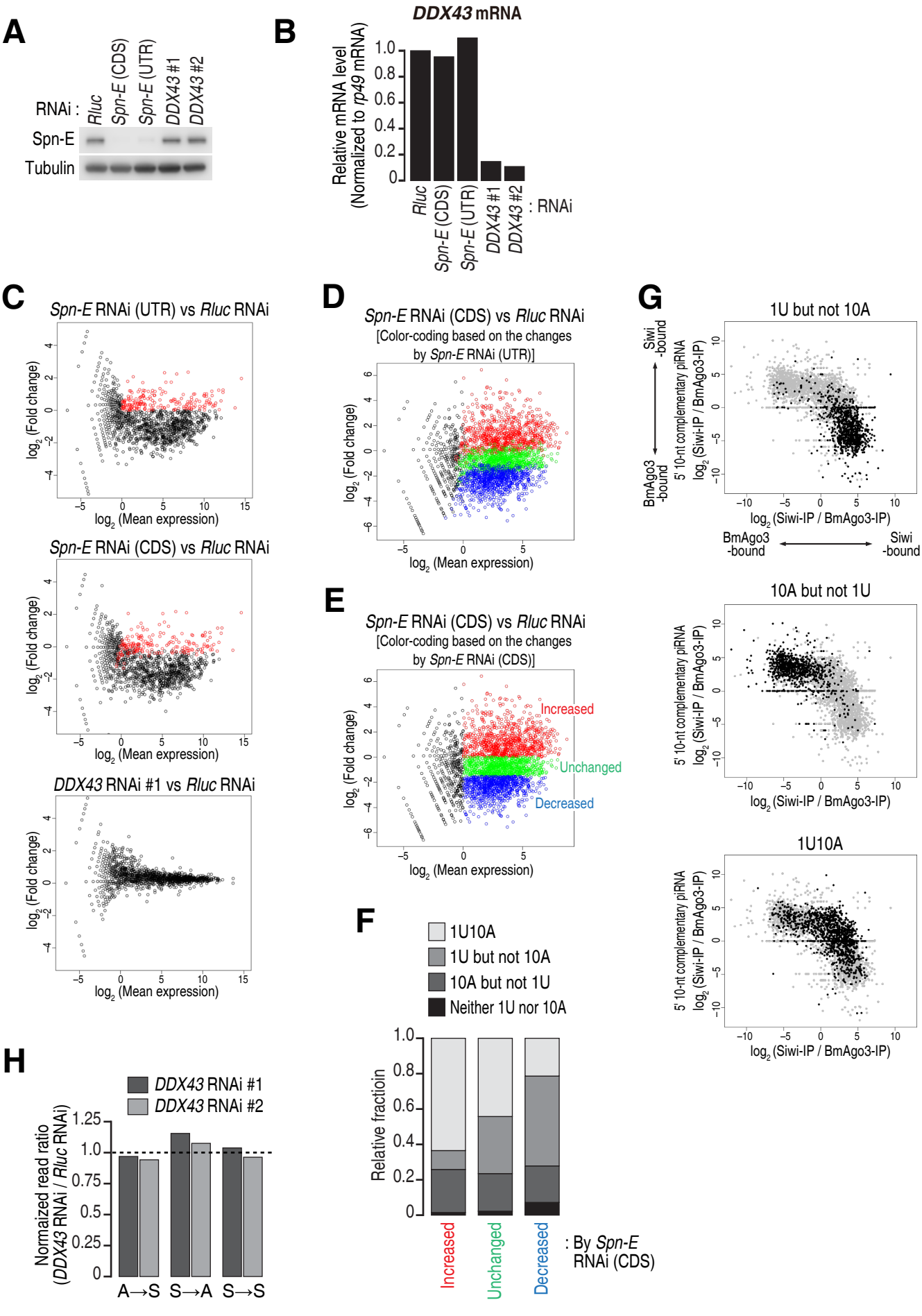
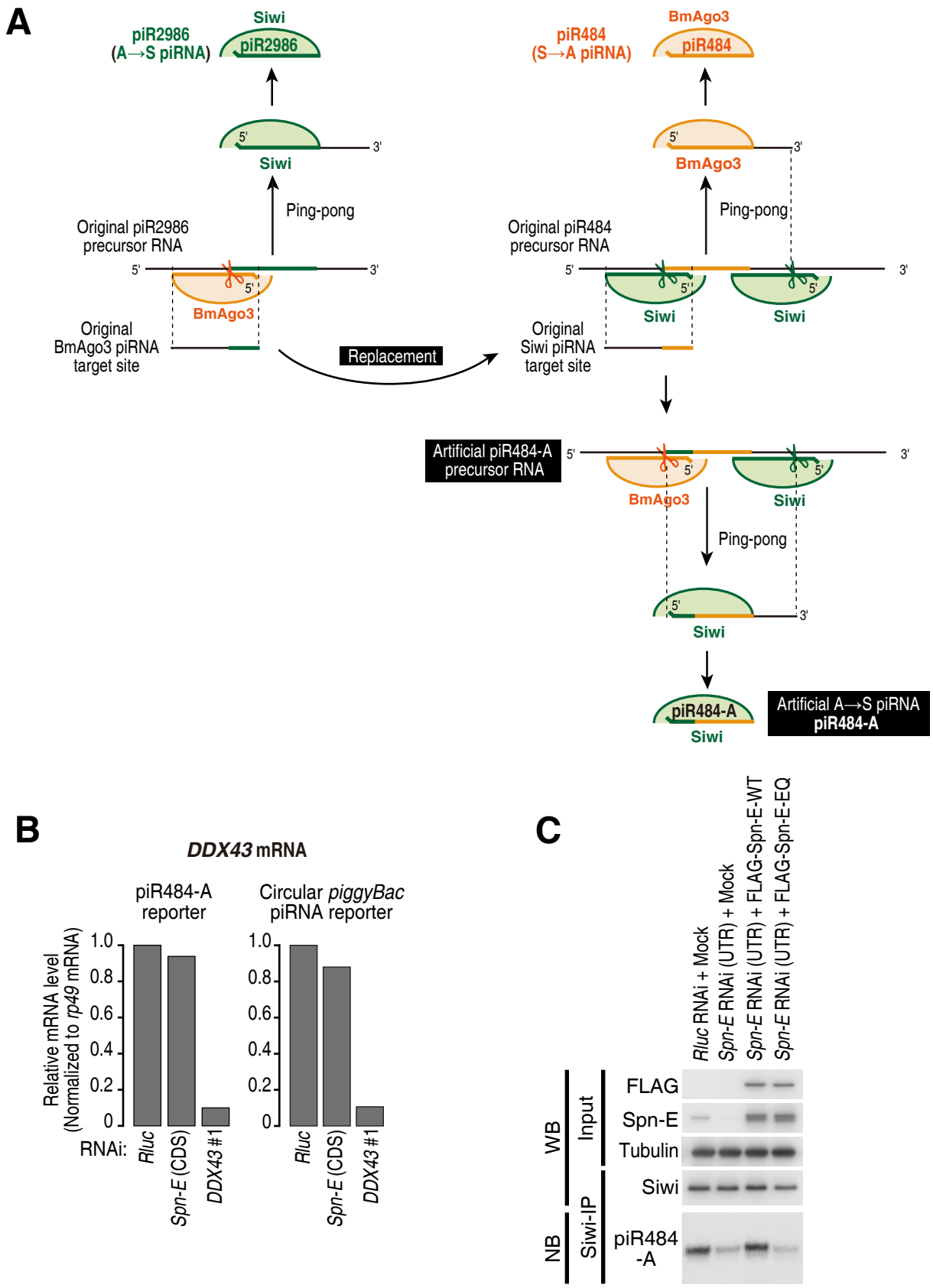

A
RNAi :
Rluc
Spn-E (CDS)
Spn-E (UTR)
DDX43 #1
DDX43 #2
Spn-E
Tubulin
B
DDX43 mRNA
Relative mRNA level (Normalized to rp49 mRNA)
: RNAi
C
Spn-E RNAi (UTR) vs Rluc RNAi
Spn-E RNAi (CDS) vs Rluc RNAi
DDX43 RNAi #1 vs Rluc RNAi
log2 (Fold change)
log2 (Mean expression)
D
Spn-E RNAi (CDS) vs Rluc RNAi
[Color-coding based on the changes by Spn-E RNAi (UTR)]
E
Spn-E RNAi (CDS) vs Rluc RNAi
[Color-coding based on the changes by Spn-E RNAi (CDS)]
Increased
Unchanged
Decreased
F
1U10A
1U but not 10A
10A but not 1U
Neither 1U nor 10A
Relative fractioin
: By Spn-E RNAi (CDS)
G
1U but not 10A
10A but not 1U
1U10A
Siwi -bound
BmAgo3 -bound
5' 10-nt complementary piRNA
log2 (Siwi-IP / BmAgo3-IP)
H
DDX43 RNAi #1
DDX43 RNAi #2
Normaized read ratio (DDX43 RNAi / Rluc RNAi)
A→S
S→A
S→S

Figure EV3


A
piR2986
(A→S piRNA)
Siwi
piR2986
5'
3'
Siwi
Ping-pong
Original piR2986
precursor RNA
5'
3'
5'
BmAgo3
Original
BmAgo3 piRNA
target site
Replacement
piR484
(S→A piRNA)
BmAgo3
piR484
5'
3'
BmAgo3
Ping-pong
Original piR484
precursor RNA
5'
3'
5'
5'
Siwi
Siwi
Original
Siwi piRNA
target site
Artificial piR484-A
precursor RNA
5'
3'
5'
5'
BmAgo3
Siwi
Ping-pong
5'
3'
Siwi
piR484-A
Siwi
Artificial A→S piRNA
piR484-A
B
DDX43 mRNA
piR484-A
reporter
Circular piggyBac
piRNA reporter
Relative mRNA level
(Normalized to rp49 mRNA)
1.0
0.8
0.6
0.4
0.2
0
RNAi:
Rluc
Spn-E (CDS)
DDX43 #1
C
Rluc RNAi + Mock
Spn-E RNAi (UTR) + Mock
Spn-E RNAi (UTR) + FLAG-Spn-E-WT
Spn-E RNAi (UTR) + FLAG-Spn-E-EQ
WB
Input
FLAG
Spn-E
Tubulin
Siwi
NB
Siwi-IP
piR484
-A